

Escherichia coli K-12 MG1655: b3738

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Entry	b3738 CDS E.coli
Gene name	atpB, ECK3731, JW3716, papD, uncB
Definition	F0 sector of membrane-bound ATP synthase, subunit A (EC:3.6.3.14)
Orthology	KO: K02108 F-type H ⁺ -transporting ATPase subunit a [EC:3.6.3.14]
Pathway	PATH: eco00190 Oxidative phosphorylation PATH: eco01100 Metabolic pathways
Class	Metabolism; Energy Metabolism; Oxidative phosphorylation [PATH:eco00190] BRITE hierarchy
SSDB	Ortholog Paralog Gene cluster GPIT
Motif	Pfam: DUF1129 ATP--synt_A PROSITE: ATPASE_A Motif
Other DBs	RegulonDB: B3738 EcoGene: EG10099 ECOCYC: EG10099 NCBI-GI: 16131606 NCBI-GeneID: 948252 UniProt: P0AB98
LinkDB	All DBs
Structure	PDB: 1C17 Thumbnail  Jmol
Position	complement(3919259..3920074) Genome map
AA seq	271 aa AA seq DB search MASENMTPQDYIGHHLNNLQLDLRTFSLVDPQNPPATFWTINIDSMFFSVVLGLLFLVLF RSVAKKATSGVPGKFQTAIELVIGFVNGSVKDMYHGKSKLIAPLALTIFVWVFLMNLMDL LPIDLLPYIAEHVLGLPALRVVPSADVNVTLSMALGVFILILFYSIKMKGIGGFTKELTL QPFNHWAFIPVNLILEGVSLLSKPVSLGLRLFGNMYAGELIFILIAGLLPWWSQWILNVP WAIFHILIIITLQAFIFMVLTIIVYLSMASEEH
NT seq	816 nt NT seq +upstream <input type="text" value="0"/> nt +downstream <input type="text" value="0"/> nt atggcttcagaaaatatgacgccgcaggattacataggacaccacctgaataaccttcag ctggacctgcgtacattctcgtcgttgatccacaaaacccccagccaccttctggaca atcaatattgactccatgttcttctcgtggtgctgggtctggtgttcctggttttattc cgtagcgtagccaaaaggcgaccagcgggtgtgccaggtaagtttcagaccgcgattgag ctggtgatcggtttgttaatggtagcgtgaaagacatgtaccatggcaaaagcaagctg attgctccgctggccctgacgatcttcgtctgggtattcctgatgaacctgatggattta ctgcctatcgacctgctgccgtacattgctgaacatgtactgggtctgcctgcactgcgt

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